OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: August 19, 2003, 15:23:30 ; Search time 467 Seconds
                                             4375.749 Million cell updates/sec

Title: US-09-494-297-2
Perfect score: 3945
Sequence: 1 MKKTRFPNKLNTLNTQRVLS.........IAGISLGIWGIHTIRIRKHD 757

Scoring table: BLOSUM62
                Xgapop   10.0 , Xgapext   0.5
                Ygapop   10.0 , Ygapext   0.5
                Fgapop   6.0 , Fgapext   7.0
                Delop   6.0 , Delext   7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgn2_1/USPTO_spool/US09494297/runat_13082003_122946_28082/app_query.fasta_1.903
-DB-N_Geneseq_19Jun03 -QFMT-fastap -SUFFIX-rng -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cd1
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-pto -NORMext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09494297_@CGN_1_1_304_@runat_13082003_122946_28082 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database :   N_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB Length	ID	Description
1	3945	100.0	2286	24	ABN69678	Streptococcus poly
2	236.5	6.0	1020	24	ABN69681	Streptococcus poly
3	196	5.0	15614	24	AAX12982	Enterococcus faeca
4	196	5.0	15614	24	ABS98777	Enterococcus faeca
5	180	4.6	2127	21	AAA30874	Streptococcus equi
6	178	4.5	7650	20	AAV82019	Moraxella catarrha
7	177	4.5	49617	22	AAF28541	Genomic fragment #
8	176	4.5	2718	20	AAV82021	Moraxella catarrha
9	161	4.1	4161	24	ABQ69442	Listeria innocua D
10	161	4.1	4185	24	ABQ67871	Listeria innocua D
11	161	4.1	4249	20	AAX20201	Enterococcus faeca
12	161	4.1	4249	20	ABN98186	Enterococcus faeca
13	161	4.1	4249	25	ABX61756	E faecalis EF104 g
14	161	4.1	4359	20	AAX20200	Enterococcus faeca
15	161	4.1	4359	24	ABN98185	E faecalis EF104 g
16	161	4.1	4359	25	ABX61755	Enterococcus faeca
17	161	4.1	12445	20	AAX13179	Enterococcus faeca
18	161	4.1	12445	24	ABS98974	Enterococcus faeca
19	161	4.1	11630020	24	ABQ67197	Listeria innocua c
20	161	4.1	3011208	24	ABQ69245	Listeria innocua D
21	159	4.0	4593	24	ABQ68111	Listeria monocytog
22	159	4.0	4593	24	ABQ70032	Listeria monocytog
23	159	4.0	2944528	24	ABA03041	Listeria monocytog
24	156	4.0	4557	24	ABK75341	Bacillus lichenifo
25	155	3.9	2499	24	ABQ68254	Listeria monocytog
26	155	3.9	2499	24	ABQ69824	Listeria monocytog
27	155	3.9	2944528	24	ABA03041	Listeria monocytog
28	154	3.9	5547	18	AAT68844	Photorhabdus lumin
29	152.5	3.9	6042	24	ABQ69231	Listeria sp DNA se
30	152	3.9	5547	19	AAV29930	tcdA gene from the
31	152	3.9	7551	18	AAT68843	Photorhabdus lumin
32	152	3.9	7551	19	AAV29928	tcdA gene from the
33	152	3.9	7551	22	AAF58778	Photorhabdus tcdA
34	152	3.9	7551	24	AAS55583	Photorhabdus (W-
35	152	3.9	7577	22	AAF58780	P. luminescens (W-
36	152	3.9	7621	22	AAF58783	Modified Photorhab
37	150	3.8	3531	20	AAX77451	TcdA toxin-zein ER
38	150	3.8	3698	24	AAD35550	S. pyogenes SFPBP-
39	149	3.8	2700	21	AAX97541	Streptococcal fibr
40	149	3.8	3945	20	AAX77593	Human Hsp72 (heat
41	149	3.8	4143	25	ABT14918	S. aureus SdrD DNA
42	149	3.8	6168	20	AAX20228	Pathogen specific
43	149	3.8	6168	20	AAX20230	Enterococcus faeca
44	149	3.8	6168	20	AAX20232	Enterococcus faeca
45	149	3.8	6168	24	ABN98213	E faecalis EF123 g

RESULT 1
ABN69678

ID   ABN69678 standard; DNA; 2286 BP.
XX
AC   ABN69678;
XX
DT   01-JUL-2002 (first entry)
XX
DE   Streptococcus polynucleotide SEQ ID NO 7269.
XX
KW   Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW   group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
KW   antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX
OS   Streptococcus pyogenes.
XX
PN   WO200234771-A2.

ALIGNMENTS

```
XX
PD   02-MAY-2002.
XX
PF   29-OCT-2001; 2001WO-GB04789.
XX
PR   27-OCT-2000; 2000GB-0026333.
PR   24-NOV-2000; 2000GB-0028727.
PR   07-MAR-2001; 2001GB-0005640.
XX
XX
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
XX
PI   Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
PI   Tettelin H;
XX
DR   WPI; 2002-352536/38.
DR   P-PSDB; ABP29047.
XX
PS   Claim 7; Page 3879; 4525pp; English.
XX
PT   New Streptococcus protein for the treatment or prevention of infection
PT   or disease caused by Streptococcus bacteria, such as meningitis, and
PT   for detecting a compound that binds to the protein .
XX
CC   The invention relates to a protein (ABP25413-ABP30895) from group B
CC   streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC   (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
CC   the specification. The proteins have antibacterial and antiinflammatory
CC   activity. (I), nucleic acids encoding (II), ABN66044-ABN71526 and
CC   antibodies that bind (I) are used in the manufacture of medicaments for
CC   the treatment or prevention of infection or disease caused by
CC   Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC   Nucleic acids encoding (II) are used to detect Streptococcus in a
CC   biological sample. (I) is used to determine whether a compound binds to
CC   (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC   used as a vaccine or diagnostic composition. The disease caused by
CC   Streptococcus that is prevented or treated may be meningitis. Nucleic
CC   acid encoding (II) may be used to recombinantly produce (I) and may be
CC   used in gene therapy. Antibodies to (I) are used for affinity
CC   chromatography, immunoassays, and distinguishing/identifying
CC   Streptococcus proteins.
XX
SQ   Sequence 2286 BP; 831 A; 347 C; 447 G; 661 T; 0 other;
```

```
Alignment Scores:
Pred. No.:             2.5e-300        Length:         2286
Score:                 3945.00         Matches:        757
Percent Similarity:    100.00%         Conservative:   0
Best Local Similarity: 100.00%         Mismatches:     0
Query Match:           100.00%         Indels:         0
DB:                    24              Gaps:           0
```

```
US-09-494-297-2 (1-757) x ABN69678 (1-2286)

Qy    1 MetLysLysThrArgPheProAsnLysLeuAsnThrLeuAsnThrGlnArgValLeuSer       20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   16 ATGAAAAAAACAAGGTTTCCAAATAAGCTTAATACTCTTAATACTCAAAGGGTATTAAGT      75

Qy   21 LysAsnSerLysArgPheThrValThrLeuValGlyValProPheLeuMetIlePheAlaLeu    40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   76 AAAAACTCAAAACGATTTACTGTCACTTTAGTGGGAGTCTTTTTAATGATCTTCGCTTTG     135

Qy   41 ValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSerThrProAsn          60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  136 GTAACTTCCATGGTTGGTGCTAAGACTGTTTTTGGTTTAGTAGAATCCCTGACCCCAAAC     195

Qy   61 AlaIleAsnProAspSerSerGluThrYrArgThrProTyrGlyTyrGluSerTyrArgVal     80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  196 GCAATAAATCCAGATTCAAGTGAAACTTATAGAACTCCATATGGTTATGAAAGTTATAGA     255

Qy   81 GlyHisProTyrTyrLysGlnPheAsnGluArgValAlaLysLeuAsnLeuGluGly          100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  256 GGGCATCCATATTATAAACAGTTTAACGAACGAGTAGCAAAGCTTAACCTTGAAGGA       315

Qy  101 SerArgSerTyrArgGlnValTyrCysPheAsnLeuLysLysAlaPheProLeuGlySerAsp    120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  316 AGTAGAAGTTATCAAGTTTATTGCTTTAATTTAAAGAAAGCATTTCCTCTCGGATCAGAT     375

Qy  121 SerSerValLysTrpTyrLysLysHisAspGlyIleSerThrLysProTyr               140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  376 AGTAGTGTTAAAAAGTGGTATAAAAACATGATGGAATCTCTACAAAATTGGAGATTAT      435

Qy  141 AlaMetSerProArgIleThrGlyArgGluLeuAsnGlnLysLeuArgAlaValMetTyr       160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  436 GCGATGAGCCCTAGAATTACGGGAGAGGAGCTAAATCAGAAGTTACGAGCTGTTATGTAT     495

Qy  161 AsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluProLeuAsnAlaIle       180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  496 AATGGACATCCACAAAATGCCAATGGTATTATGGAAGGCTTGGAACCCTTGAATGCTATC     555

Qy  181 ArgValThrGlnGluValAlaValTrpTyrTyrLysSerAspAsnAlaProIleSerAsnProAsp 200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  556 CGTGTAACTCAAGAGGTTGCAGTCTGGTATTATAAATCTGATAATGCTCCTATTTCAAATCCTGAT 615

Qy  201 GluSerPheLysArgGluSerGlySerAsnLeuValSerThrSerGlnLeuSerLeuMet       220
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  616 GAAAGTTTTAAAAGGGAGTCAGGAAGTAACTTGGTTAGTACTTCTCAATTATCTTTGATG     675

Qy  221 ArgGlnAlaLeuLysGlnLeuIleLeuGluAspProAsnLeuAlaThrLysMetProLysGlnVal 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  676 CGTCAAGCTTTGAAGCAACTGATTTTAGAAGATCCTAATTTAGCTACAAAAATGCCAAAAGGT  735

Qy  241 ProAspProAspPheGlnIleLeuSerIlePheGluSerGluGluArgGlyAlaAspLysTyrAsnLys 260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  736 CCGGATCCAGATTTTCAGCTAAGTATATTTGAGTCTGAGGAACGAGGAGATAAAATATAAAA    795

Qy  261 GlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThrThrLysProProGlyAsp         280
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  796 GGATACCAAAATCTTTTGAGTGGTGGTTTAGTTCCTACTACAAAACCACCAGGAGAC        855

Qy  281 ProProMetProProAsnGlnProGlnThrThrSerValLeuIleLeuArgLysTyrAlaIle    300
        |||||||||||||||||||||||||||||||||||N||||||||||||||||||||||||
Db  856 CCACCAAATGCCTCCAAATCAACCTCAGACTACTTCAGTACTTATTAGAAAGTATGCTATA     915

Qy  301 GlyAspTyrSerLysLeuLeuGluGlyValAlaThrLeuGluThrGlyAspAsnValAsn       320
        ||||||||||||||||||||||||||||||||||N||||||||||||||||||||||||
Db  916 GGTGATTACTCTAAATTGCTTGAAGGTGCAACATTAGAGACAGGGGATAACGTGAAT       975

Qy  321 SerPheGlnAlaArgValPheSerSerAsnAspIleGluGlyArgIleGluLeuSerAsp       340
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  976 AGTTTTCAACCGAGAGTGTTTAGCAGTAATGATATTGAAGGAAGAATCGAACTATCAGAT    1035

Qy  341 GlyThrThrTyrPheLeuThrGlnAsnTyrLeuAsnSerProAlaGlyTyrSerIleAlaGluProIle 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1036 GGAACTACTTATTTCTTTAACTGAATTGAATTCTCCAGCTGGTTATAGTATCGCAGAGCCAATC 1095

Qy  361 ThrPheLeuLysThrGlnLysValGlyLeuGlyLysGlyLysGluLeuGluAsn            380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1096 ACTTTTTTAAAGTGAAGCTGGCAAAGTGTAACATAGTATATGATGGAAAAACAGATTGAAAAT 1155

Qy  381 ProAsnLysGluIleValGluProTyrSerValGluLeuAlaTyrAsnAspPheGluGluPhe    400
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1156 CCCAATAAAGAAATAGTAGAGCCTTACTCAGTAGAGCTAGCATATAATGATTTGAAGAATTT  1215

Qy  401 SerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySer       420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1216 AGCGGTTTAACTACACAAAACTATGCAAAATTTTATTATGCCAAAAATAAAAAATGGAAGT    1275

Qy  421 SerGlnIleValValTyrCysPheAsnAlaAspLeuGlySerProProAspSerGluAspGly    440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1276 TCACAGGTTGTCGTTATTGCTTTAATGCAGATCTAAAATGTCCACCAGACTCTGAAGATGGT   1335

Qy  441 GlyLysThrMetThrProAspPheThrThrGlyLeuValLysTyrThrHisIleAlaAlaGly    460
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1336 GGGAAAACAAATGACTCCCAGACTTTCACAACAGGAGAAGTAAAATCAACACTCATTGCAGGT  1395
```

```
Qy   461 ArgAspLeuPheLysTyrThrValLysProArgAspThrAspPheLeuLys 480
Db  1396 CGTGACCTCTTTAAATATACTGTGAAACCAAGAGATACCGATCCTGACATTTCTTAAA 1455

Qy   481 HisIleLysLysValIleGluLysGlyTyrArgGlyLysGlyGlnAlaIleGluTyrSer 500
Db  1456 CATATCAAAAAAGTAATTGAGAAGGGTTACAGGGAAAAAGGACAAGCTATTGAGTAPAGT 1515

Qy   501 GlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIleIleTyrTyrPheThrAsp 520
Db  1516 GGTCTAACTGAGACACAATTGCGTGCGGCTACTCAGTTAGCAATATTATTATTCACTGAT 1575

Qy   521 SerAlaGluLeuAspLysAspTyrHisGlyPheGlyAspMetAsnAsp 540
Db  1576 AGTGCTGAATTAGATAAGGATTAAACTACTCATGGTTTGGAGACATGAATGAT 1635

Qy   541 SerThrLeuAlaAlaIleAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProProGln 560
Db  1636 AGTACTTTAGCAGTTGCTAAAAACCTTGTAGAATACGGCTCAAGATAGTAGTTAATCCTCACAG 1695

Qy   561 LeuThrAspLeuAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAlaAspArgThr 580
Db  1696 CTAACTGACCTTTGATTTCTTTATTCTTAGAACAAAATATGAATTCATTAGGTTACAC 1755

Qy   581 GlnTrpHisProGluAspLeuValAlaAspIleIleArgMetGluAspLysLysGluValIle 600
Db  1756 CAGTGGCATCCAGAAGATTTAGTTGCATATTATTCGTTATGGAAGATAAAAAAAGAAGTTATA 1815

Qy   601 ProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAlaAspArgThr 620
Db  1816 CCTGTAACTCATAATTTAACATTAAGAAAAACGGTGACTGGTTTACCTGGTGACAGAACT 1875

Qy   621 LysAspSerPheHisSerGluIleGluLeuLysAspAsnAsnLysGlnLeuLeuSerGlnThr 640
Db  1876 AAAGATTTCCATTTGAAATTGAAATTAAAGGATAATAAAGCCAAGAATTGCTTTCTCAAACT 1935

Qy   641 ValLysThrAspSerLysThrAspSerAsnLeuGluPheLysLysSerAlaThrIleAsnLeu 660
Db  1936 GTTAAAACAGATAAAAATACAAACCTCGAATTTAAAAAGAGTGCAAGCGATAAATTAATTTAAAA 1995

Qy   661 HisGlyGluSerLeuThrLeuGlnGlyLeuProGluGluLeuArgSerTyrLeuValLysGlu 680
Db  1996 CATGGGGAAAGTTTAACACTTCAAGGTTTACCAGAAGAAGTTAGTCTTACCTTGTCAAAGAA 2055

Qy   681 ThrAspSerSerGluGlyTyrArgLysValAsnSerGlnGluValAlaAlaAsnAlaThrVal 700
Db  2056 ACAGATTCTGAAGGCTGTATAAGGTTAAATGCACAAAATGCTACAGTT 2115

Qy   701 SerLysThrThrGlyIleIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGlyProVal 720
Db  2116 TCAAAAACAGGAATAAACAAGTGATGAGACACTTGCTTTTGAAAAATAATAAAGGCCTGTT 2175

Qy   721 ValProThrGlyValAspSerGlnIleLysAsnGlyTyrTyrLeuAlaLeuIleValAlaGly 740
Db  2176 GTTCCTACAGGAGTTGATCAAAGATCAATGGCTATCTAGCTTTGATAGTTATCGCTGGT 2235

Qy   741 IleSerLeuGlyIleLeuTrpIleGlyIleLeuHisThrIleArgIleAspArgLysHisAsp 757
Db  2236 ATCAGTTTGGGGATCTGGGGAATTCACACGATAAGGATAAGAAAAACATGAC 2286
```

RESULT 2
ABN69681
ID   ABN69681 standard; DNA; 1020 BP.
XX
AC   ABN69681;
XX
DT   01-JUL-2002 (first entry)
XX
DE   Streptococcus polynucleotide SEQ ID NO 7275.
XX
KW   Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW   group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
KW   antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX
OS   Streptococcus pyogenes.
XX
PN   WO200234771-A2.
XX
PD   02-MAY-2002.
XX
PF   29-OCT-2001; 2001WO-GB04789.
XX
PR   27-OCT-2000; 2000GB-0026333.
PR   24-NOV-2000; 2000GB-0028727.
PR   07-MAR-2001; 2001GB-0005640.
XX
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
XX
PI   Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
PI   Tettelin H;
XX
DR   WPI; 2002-352536/38.
DR   P-PSDB; ABP29050.
XX
PT   New Streptococcus protein for the treatment or prevention of infection
PT   or disease caused by Streptococcus bacteria, such as meningitis, and
PT   for detecting a compound that binds to the protein -
XX
PS   Claim 7; Page 3880; 4525pp; English.
XX
CC   The invention relates to a protein (ABP25413-ABP30895) from group B
CC   streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC   (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
CC   the specification. The protein have antibacterial and antiinflammatory
CC   activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC   antibodies that bind (I) are used in the manufacture of medicaments for
CC   the treatment or prevention of infection or disease caused by
CC   Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC   Nucleic acids encoding (I) are used to detect Streptococcus in a
CC   biological sample. (I) is used to determine whether a compound binds to
CC   (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC   used as a vaccine or diagnostic composition. The disease caused by
CC   Streptococcus that is prevented or treated may be meningitis. Nucleic
CC   acid encoding (I) may be used to recombinantly produce (I) and may be
CC   used in gene therapy. Antibodies to (I) are used for affinity
CC   chromatography, immunoassays, and distinguishing/identifying
CC   Streptococcus proteins.
XX
SQ   Sequence 1020 BP; 375 A; 162 C; 196 G; 287 T; 0 other;

US-09-494-297-2 (1-757) x ABN69681 (1-1020)

Alignment Scores:

Pred. No.:	1.83e-09	Length:	1020
Score:	236.50	Matches:	96
Percent Similarity:	40.43%	Conservative:	54
Best Local Similarity:	25.88%	Mismatches:	118
Query Match:	5.99%	Indels:	103
DB:	24	Gaps:	16

US-09-494-297-2 (1-757)

```
Qy   404 ThrThrGlnAsnThrTyrAlaLysPheTyrTyrAlaLysLysAsn------GlySerSer 421
             |||  :::   ||||||     ||||::
Db    73 ACTGTTGTAAACGAGAGCCAAACTAACAGTTACAAAAAACCTTGATTTAGTTAATAGCAAT 132

Qy   422 GlnValValTyrCysPheAsnAlaAspLeuLysSerProProAsp------SerGlu 438
             ::::::    ::      |||
Db   133 GCATAATTCCAAATACAGATTTACATTTAAAAATCGAACCTGATACTACTGTCAACGAA 192

Qy   439 AspGlyGlyTyrLysThrMetThrProAspPheThrThrGlyLeuValLysTyrThrHisIle 458
             ||||| ||||||   |||  :::
Db   193 GACGGAAATAAGTTAAAGGTGTTAGCTTTCGAACACACCGATGACTAAAGTCACTTAC--- 249

Qy   459 AlaGlyTyrArgAspLeuPheLysTyrThrValLysProArgAspThrAspThrPhe 478
             ||:::  |||
Db   250 --------ACCAATTCAGAT------ 261
```